Attorney Docket No.: ISIS - 10450

Client Docket No.: DIBIS-0002US.P3

IN THE CLAIMS

1, - 29. (cancelled)

30. (previously presented) A method of identifying a virus comprising: contacting nucleic acid from said virus with at least one pair of primers which hybridize to flanking sequences of said nucleic acid, wherein said flanking sequences flank a variable nucleic acid sequence of said virus;

amplifying said variable nucleic acid sequence to produce an amplification product;

determining the base composition of said amplification product by mass spectrometry, wherein said base composition identifies the number of A residues, C residues, T residues, G residues, U residues, analogues thereof and mass tag residues thereof in said amplification product; and

comparing said base composition of said amplification product to calculated or measured base compositions of analogous amplification products of one or more known viruses present in a database comprising 5 or more base compositions with the proviso that sequencing of said amplification product is not used to identify the virus.

- 31. (previously presented) The method of claim 30, further comprising repeating said contacting, amplifying, determining and comparing steps using one or more additional pairs of primers.
- 32. (previously presented) The method of claim 30, wherein said virus is a biological warfare threat agent.
- 33 (previously presented) The method of claim 30, wherein said virus is identified at the sub-species level.

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34 - 49. (cancelled).

50. (previously presented) The method of claim 30, wherein said virus is a

respiratory pathogen.

51. (previously presented) The method of claim 30, wherein said virus is a hepatitis

C virus.

52. (previously presented) The method of claim 30, wherein said virus in an

immunodeficiency virus.

53. (currently amended) The method of claim 30, wherein said virus is a member of a

viral family selected from the group consisting of Filoviridae, Flavifiridae, Arenaviridae,

Bunya viridae, Adenoviridae, Picorna viridae, Toga viridae, and Corono a viridae.

54. (previously presented) The method of claim 56, wherein said housekeeping gene is a polymerase, a virion component, a helicase, a protease, a methyltransferase, or an

accessory protein.

55. (previously presented) The method of claim 54, wherein said polymerase is

RNA-dependent RNA polymerase, DNA-dependent DNA polymerase or DNA-

dependent RNA polymerase.

56. (previously presented) The method of claim 30, wherein said nucleic acid is a

housekeeping gene.

57. (previously presented) The method of claim 30, wherein said amplifying step

comprises the polymerase chain reaction.

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58. (previously presented) The method of claim 30, wherein the sequences to which the primers hybridize are separated by between about 60-100 nucleotides.

- 59. (previously presented) The method of claim 30, wherein said virus is identified at the species level.
- (previously presented) The method of claim 30, wherein said pair of primers comprises at least one nucleotide analog.
- 61. (previously presented) The method of claim 60, wherein said nucleotide analog is inosine, uridine, 2.6-diaminopurine, propyne C, or propyne T.
- 62. (previously presented) The method of claim 30, wherein a molecular mass-modifying tag is incorporated into said amplification product to limit the number of possible base compositions consistent with the mass of said amplification product.